

The Highly Interactive Data Analysis Platform (HIDAP)

HIDAP, a better tool than Clone Selector for breeders to design and manage their trials, has been launched in 2017.

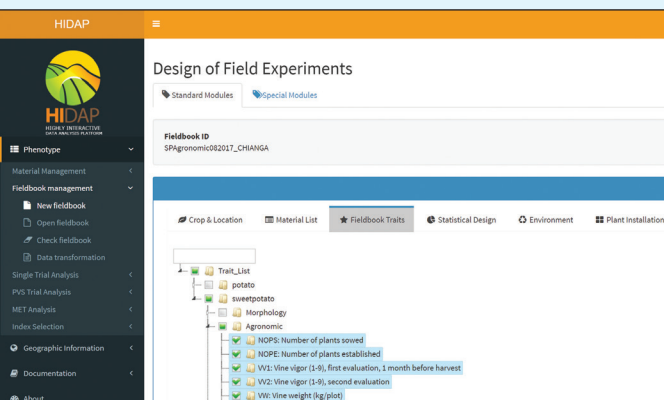


Fig. 1 Design of field experiment page in HIDAP program

➤ What is the problem?

Breeding programs involve large investments of time and money, but can pay very large returns on investment in the form of improved varieties which benefit farmers, societies and the environment. International breeding efforts involving multiple partners and targeting regionally important constraints have great potential for efficiently and rapidly achieving impact. Standardized information on the performance of progenies and selected clones across environments assists breeders to efficiently make decisions about selection and ultimately, release of new varieties. Standardized methods also facilitate sharing and reporting of breeding program results with colleagues and the agencies that support us. Several tools already exist to help with standardised breeding information management. For clonal crop breeders, the challenge has been how to improve the usability and power of existing tools, leveraging on advancements in various open source software technologies in the breeding space. The Highly Interactive Data Analysis Platform (HIDAP) has been developed to address the above challenge.

➤ What do we want to achieve?

HIDAP has been developed by the International Potato Center (CIP). It is part of on-going in-house efforts to unify best practices among breeders at CIP and national research programs.

These practices include how to best design trials (Fig.1), collect data from trials, assure data quality and conduct the proper data analysis in clonal crop breeding. HIDAP builds on the former in-house tools DataCollector and CloneSelector. DataCollector was used by potato breeders. CloneSelector was used by sweetpotato breeders since 2010. HIDAP now provides a single platform for use by potato and sweetpotato breeders, as well as improved usability and data quality checks. It also has new features built to support compliance with Open Access, open standards such as the potato and sweetpotato crop ontologies and linkages with relevant corporate and community databases, for example, CIP's Corporate Database (<https://research.cip.cgiar.org/gtdms/biomart>) and the SweetPotatoBase (www.sweetpotatobase.org) developed by the Boyce Thompson Institute.

➤ Where are we working?

HIDAP is a software tool for use by clonal crop breeders within CIP and its partners around the world. It was developed at CIP headquarters in Lima, Peru and tested in the African region.

➤ How are we going to make it happen?

HIDAP builds on the statistical platform R. This includes the R shiny tools, the knitr package, the agricolae package, and more than 100 other R packages. HIDAP re-uses the R code developed for DataCollector and CloneSelector. The R shiny package enables implementation of interactive web pages that are usable online and offline. The knitr package enables the creation of reproducible reports (Fig. 2). The statistical analysis is performed using R and R functions developed at CIP. The current version of the software is available for public use and can be downloaded at <https://research.cip.cgiar.org/gtdms/hidap/>.

Key features of HIDAP include:

1. Entirely Open Source meaning no license fees need to be paid.
2. Easy to install. End users can download a

2.3.3. Plot of means
It is always good to have some visualization of the data. Because the number of genotypes in your experiment is not so big, we can plot the data for each genotype:
DOTPLOT WITH MEANS +/- 1 STANDARD DEVIATIONS

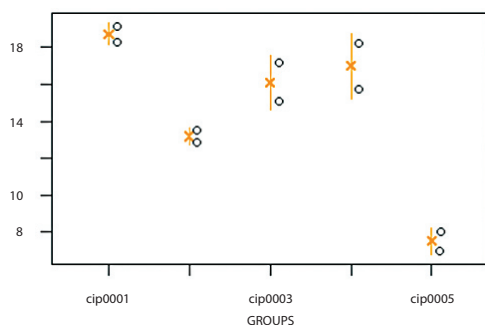


Fig. 2 Excerpt from results report generated by HIDAP

stable release of the software and follow a friendly graphical interface to complete the set up. This is a clear improvement over much more complex installation process required by CloneSelector.

3. Provides a unified platform for breeders of different clonal crops.
4. Supports offline usage. Online usage has been successfully tested and will be ready in 2018.
5. Can read information (pedigree and passport genotypes) from CIP's Corporate Database (<https://research.cip.cgiar.org/gtdms/biomart/>). The experimental data can also be uploaded to the database via the Field Book Registry Tool (<https://research.cip.cgiar.org/gtdms/fieldbook>) and can be published in Open Access through CIP's Dataverse (<https://data.cipotato.org>).
6. Has an improved web based user interface, making it easy to present users with a more refined look and feel compared to the Excel-based interfaces of CloneSelector and DataSelector.
7. Has improved usability and data quality checks.
8. Supports design of field experiments under several different experimental designs.
9. Supports creation of FieldBooks, which can be manipulated using Excel.
10. Supports analysis of single and multi-environment experiments.
11. Permits custom analysis providing reproducible reports, available in both MS Word and HTML formats.

➤ Who are we working with?

In Africa, CIP breeders at the three Sweetpotato Support Platforms (SSPs) in Uganda, Mozambique and Ghana have received training and are using the software. CIP will also provide technical backstopping on how to use the program to national breeding programs in at least 14 target countries for the Sweetpotato for Health Initiative (SPHI). HIDAP has been

developed with the support of Genomic Tools 4 Sweetpotato Improvement project (GT4SP), The United States Agency for International Development (USAID), the CGIAR Research Program on Roots, Tubers & Bananas (RTB) and the Sweetpotato Action for Security and Health in Africa (SASHA) project.

➤ What have we achieved so far?

The first stable release of HIDAP was done early 2017, followed by 2 major updates in July 2017. Most of the major functionalities are now stable. A series of introductory webinars were done to introduce the software to endusers, with participation limited initially to CIP researchers. Reference manuals and training materials from the introductory webinars are available for download to the public on the HIDAP website above.

In May 2017, 27 sweetpotato breeders from across SSA participated in a one-and-a-half-day training on the use of HIDAP during the annual sweetpotato breeders meeting in Kigali, Rwanda. Follow up in-country trainings were held in July and August 2017 for sweetpotato breeders and technicians based at Ethiopia's Southern Agricultural Research Institute (SARI) and Tigray Agricultural Research Institute (TARI) and Tanzania's Ukiriguru Agriculture Research Institute (LZARDI) (Fig. 3). In-country trainings allow for more in-depth discussions than is possible at the annual breeders meeting, and participation by a wider audience from the participating breeding programs.

➤ What's next?

The development of HIDAP is led by the Research Informatics Unit (RIU), based at CIP headquarters in Lima, Peru. Enduser feedback from both within CIP and external partners informs a lot of the development work. A key next step is to improve the inter-connectivity between HIDAP and SweetpotatoBase drawing on Breeding API (BrAPI) standards. Another focus area includes the integration of mobile data collection.



Fig. 3 HIDAP training held for breeders in Tanzania (credit L. Laizer)

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